OM protein - protein search, using sw model

Run on: December 15, 2003, 16:51:32   Search time 37 Seconds
                   Copyright (c) 1993 - 2003 Compugen Ltd.
                                GenCore version 5.1.6
                                  (without alignments)
                        2397.681 Million cell updates/sec

Title: US-09-886-954A-1
Perfect score: 2457
Sequence: 1 MTPEDPEETQPLLGPPGGSA..........CVPEIKGKTLEQITAHPESR 477

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Databases :   Published Applications AA.*

  1: /cgn2_6/pcdata/1/pubpaa/US07_PUBCOMB.pep:*
  2: /cgn2_6/pcdata/1/pubpaa/PCT_NEW_PUB.pep:*
  3: /cgn2_6/pcdata/1/pubpaa/US09B_PUBCOMB.pep:*
  4: /cgn2_6/pcdata/1/pubpaa/US06_PUBCOMB.pep:*
  5: /cgn2_6/pcdata/1/pubpaa/US07_NEW_PUB.pep:*
  6: /cgn2_6/pcdata/1/pubpaa/PCT5_PUBCOMB.pep:*
  7: /cgn2_6/pcdata/1/pubpaa/US08_NEW_PUB.pep:*
  8: /cgn2_6/pcdata/1/pubpaa/US08_PUBCOMB.pep:*
  9: /cgn2_6/pcdata/1/pubpaa/US09B_PUBCOMB.pep:*
 10: /cgn2_6/pcdata/1/pubpaa/US09C_PUBCOMB.pep:*
 11: /cgn2_6/pcdata/1/pubpaa/US06_PUBCOMB.pep:*
 12: /cgn2_6/pcdata/1/pubpaa/US09_NEW_PUB.pep:*
 13: /cgn2_6/pcdata/1/pubpaa/US10A_PUBCOMB.pep:*
 14: /cgn2_6/pcdata/1/pubpaa/US10B_PUBCOMB.pep:*
 15: /cgn2_6/pcdata/1/pubpaa/US10C_PUBCOMB.pep:*
 16: /cgn2_6/pcdata/1/pubpaa/US10_NEW_PUB.pep:*
 17: /cgn2_6/pcdata/1/pubpaa/US6_NEW_PUB.pep:*
 18: /cgn2_6/pcdata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2457	100.0	477	12	US-10-168-651-1	Sequence 1, Appli
2	948	38.6	507	15	US-10-157-013-359	Sequence 359, App
3	723	29.4	598	14	US-10-051-909-38	Sequence 38, Appl
4	683.5	28.0	501	14	US-10-051-909-36	Sequence 359, Appl
5	615	25.0	483	15	US-10-051-909-36	Sequence 5, Appl
6	615	25.0	488	15	US-10-120-528-5	Sequence 5, Appl
7	615	25.0	488	15	US-10-161-012-46	Sequence 46, Appl
8	615	25.0	488	15	US-10-062-960B-4	Sequence 4, Appl
9	615	25.0	488	15	US-10-142-624-4	Sequence 4, Appl
10	613.5	25.0	487	15	US-09-795-693-27	Sequence 27, Appl
11	613.5	25.0	487	12	US-10-191-139-45	Sequence 45, Appl
12	613.5	25.0	487	15	US-10-156-239-27	Sequence 27, Appl
13	613.5	25.0	487	15	US-10-156-239-27	Sequence 27, Appl
14	613.5	25.0	487	15	US-10-199-485-27	Sequence 27, Appl
15	603	24.5	472	12	US-10-154-419-79	Sequence 79, Appl

ALIGNMENTS

	Score	% Query Match	Length	DB	ID	Description
16	603	24.5	472	12	US-10-146-733-74	Sequence 74, Appl
17	603	24.5	472	14	US-10-024-623-29	Sequence 29, Appl
18	598	24.3	486	9	US-09-860-232A-7	Sequence 7, Appl
19	591.5	24.1	464	12	US-10-154-419-78	Sequence 78, Appl
20	591.5	24.1	464	12	US-10-146-733-73	Sequence 73, Appl
21	591.5	24.1	464	14	US-10-024-623-28	Sequence 28, Appl
22	588.5	24.0	535	15	US-10-795-693-20	Sequence 20, Appl
23	588.5	24.0	535	15	US-10-156-239-20	Sequence 20, Appl
24	578.5	24.0	494	15	US-10-081-987A-5	Sequence 5, Appl
25	570.5	23.2	496	12	US-10-341-434-89	Sequence 89, Appl
26	568	23.1	464	12	US-10-051-909-34	Sequence 34, Appl
27	546.5	22.1	571	14	US-10-099-322-125	Sequence 125, Appl
28	543	22.0	522	12	US-10-099-322-124	Sequence 124, Appl
29	543	22.0	522	12	US-10-099-322-123	Sequence 123, Appl
30	542.5	22.1	522	12	US-10-099-322-122	Sequence 122, Appl
31	541.5	22.0	509	10	US-09-981-947A-6	Sequence 6, Appli
32	536	21.8	509	10	US-09-981-947A-6	Sequence 6, Appli
33	533	21.7	519	9	US-10-259-165-248	Sequence 248, App
34	529	21.5	492	12	US-09-205-658-208	Sequence 208, App
35	529	21.5	492	12	US-09-205-658-208	Sequence 208, App
36	529	21.5	492	12	US-10-164-419-52	Sequence 52, Appl
37	522	21.2	617	12	US-10-164-419-52	Sequence 52, Appl
38	522	21.2	617	14	US-10-144-733-47	Sequence 47, Appl
39	522	21.2	471	9	US-09-778-927A-47	Sequence 47, Appl
40	521.5	21.2	501	9	US-09-778-927A-48	Sequence 48, Appl
41	521.5	21.2	501	10	US-09-738-626-3703	Sequence 3703, Ap
42	519	21.1	491	10	US-09-738-626-3703	Sequence 3703, Ap
43	516.5	21.0	524	9	US-11-328-198-3	Sequence 3, Appli
44	513	21.0	524	12	US-09-981-332-34	Sequence 34, Appl
45	513	20.9	524	12	US-10-099-322-121	Sequence 121, App

US-10-168-651-1

Query Match   100.0%;   Score 2457;   DB 13;   Length 477;
Best Local Similarity 100.0%;   Pred. No. 1.4e-208;
Matches   477;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy     1  MYTEPDPEETCQPLLGPPGQSPAPRGRVRVTPLAAPRAAALGGPLSKGFPALGYSSPAIPSLQRAAPP   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MYTEPDPEETCQPLLGPPGQSPAPRGRVRVTPLAAPRAAALGGPLSKGFPALGYSSPAIPSLQRAAPP   60

Qy    61  APRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFVAVITAAQDV  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  APRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFVAVITAAQDV  120

Qy   121  WMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILAYLLAGWVLE  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  WMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILAYLLAGWVLE  180

Qy   181  WRWLANVLAGCVPFSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFWRGSEQCWHEDPPIGAR  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  WRWLANVLAGCVPFSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFWRGSEQCWHEDPPIGAR  240

Qy   241  QSFHLALRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYSSQIFESAKFKDSSLASVVVGV   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  QSFHLALRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYSSQIFESAKFKDSSLASVVVGV   300

Qy   301  IQVLFTAVVALIMDRAGRRLLLVLSGVVMVWTSRAPVYKLTQQGPGNSSVRAISAPVS  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  IQVLFTAVVALIMDRAGRRLLLVLSGVVMVWTSRAPVYKLTQQGPGNSSVRAISAPVS  360

Qy   361  AQPVDASVGLAWLAVGSMCLPIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLM  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  AQPVDASVGLAWLAVGSMCLPIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLM  420

Qy   421  AFLVTKEFSSLMEVLRPYGAFWLASARCITRSVLFTLFCVPETKGKTLEQITPAHFEGR  477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AFLVTKEFSSLMEVLRPYGAFWLASARCITRSVLFTLFCVPETKGKTLEQITPAHFEGR  477
```

RESULT 2

US-10-157-031-359

; Sequence 359, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Kozhesher, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 507
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-157-031-359

Query Match   38.6%;   Score 948;   DB 15;   Length 507;
Best Local Similarity 42.7%;   Pred. No. 3e-75;
Matches   216;   Conservative   80;   Mismatches   166;   Indels   44;   Gaps   11;

```
Qy    10  QPLLG--------------------PPGQSAPRGR--------RVPLAAFAAALGPLSFGFALGYSSPA   50
          ||||                      :::: |||:           :|::   |  |::  ||:
Db     3  EPLLGAEGDVDVDTEKPFPPQPSGPRGRANVGTLCNKRVFLATPAVLGNFSFGYVLVYSPV   62

Qy    51  IPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAG  110
          |||||  :::||||||||||: :::    ||||||||||||||||||||:|:||||:|||
Db    63  IPSLQRQAAFPAPRLDDAAASWFGGISILDLSWFGSVGTLGAAGGLSAMILNDLLGRKLSIMFSAVTSAAG  122
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RESULT 3

US-10-051-909-38

; Sequence 38, Application US/10051909
; Publication No. US20020192174A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen
; APPLICANT: Hitz, William
; APPLICANT: Helm, Serie, Tim
; APPLICANT: Hitz, Bill
; APPLICANT: Kinney, Tony
; APPLICANT: Tingey, Scott
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BD1163
; CURRENT APPLICATION NUMBER: US/10/051,909
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: April 24, 1998
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 501
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Oryza sativa

US-10-051-909-38

Query Match   29.4%;   Score 723;   DB 14;   Length 501;
Best Local Similarity 35.6%;   Pred. No. 2.2e-55;
Matches   173;   Conservative   89;   Mismatches   172;   Indels   52;   Gaps   8;

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Qy    17  GGSAPRGRRVRVTPLAFA-----------------AALGPLSFGFPALGYSSPAIPSLQRAAPAPAP   62
          |||||::|   ||:::                    ::|| : |::|   |: ::| ||||:||:
Db    39  GGGGSWGSRLGSSASYSLRDSSVSAVLCTIVALGPIQFGFGGFTCGFSSPV-----QDAIISDL   94

Qy    63  RLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFVAVITAAQDVWM  122
          :||||:|||  ::|:||::||||||: :||||||::|| :||:  |:||: ::|||:: |:
Db    95  GLTLSRSGLRGSLSNVGAMVGAILSGCOLAEYIGRKCGSLMIAAIENTIGWLAISFAKDSSF  154

Qy   123  LLGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILAYLLAGWVLEMR   182
          |||||:||| ||:|::||||:|:|:   |:|||| ::| :::|:|::||||||||:|:::
Db   155  LLGRLLGQFGVGVSIVVPVYIAEIAPACYRGALGLSGVNQLSVTVGILLAYLLGMFVPWR   214

Qy   183  WLANLGCVPFSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFWRGSEQCWHEDPPIGAR  240
          ||::::|||  ::::  ::|:: |:|:| | :|::|::::| |  |    : ::: : |:
Db   215  ILSVLGILPCSLILPGLPFFPESPRWLAKMGRWEDFESSSLQVLRGEE-------TDIAVEVN   269
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